



SEQUENCE LISTING

<110> Porro, Danilo
Branduardi, Paola
Valli, Minoska
Alberghina, Lilia

<120> Process for Expression and Secretion of
Proteins by the Non-Conventional Yeast *Zygosaccharomyces*
Bailii

<130> 3912.1000-000

<140> 10/534,171
<141> 2005-05-06

<150> PCT/EP2003/012377
<151> 2003-11-06

<150> 102 52 245.6
<151> 2002-11-07

<160> 95

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gtgcaagaaa accaaaaaagc aacaacaggt tttggataag tacatatata agagggcctt 180
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-65 -60 -55
Ile Pro Ala Glu Ala Val Ile Gly Tyr Leu Asp Leu Glu Gly Asp Phe -40
-50 -45 -40
Asp Val Ala Val Leu Pro Phe Ser Asn Ser Thr Asn Asn Gly Leu Leu -25
-35 -30 -25
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-20 -15 -10
Ser Leu Asp Lys Arg
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gct 63

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<220>
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tcttagtgtt cggct 75

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<220>
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<222> (1)...(17)

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gca 63

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<212> DNA
<213> Arxula adeninivorans

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<210> 22
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<213> Arxula adeninivorans

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<222> (1)...(18)

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Asp Ser

<210> 23
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<212> DNA
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Tyr Ser

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<222> (1)...(63)

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<220>
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<221> SIGNAL
<222> (1)...(23)

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<213> *Saccharomyces cerevisiae*

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<400> 42

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<220>
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<210> 47
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<210> 49
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<213> *Aspergillus niger*

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<211> 18
<212> PRT
<213> Aspergillus niger

<220>
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<220>
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Lys Ile Ser Ala
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<213> *Saccharomyces cerevisiae*

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<222> (1)...(21)

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Asn Ser Ala Leu Gly
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<213> *Saccharomyces cerevisiae*

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ggt 63

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Asn Ser Ala Leu Gly
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ttggtccttt cgcttctatt taactcagct ttgggt 96

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<220>
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-15 -10 -5

<210> 59
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<212> DNA
<213> Zygosaccharomyces bailii

<220>
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gct 63

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<213> Zygosaccharomyces bailii

<220>
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gaagaaaattt ttacagattt gacgtatcac attcacgtta acgtcagtgg cgaaattgac 180
tcttactatc ataatttagt caatttgtc gataacgctc tagcaaacaa agatattaat 240
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tacttaaatc attacgattc agagacttgc aaagatatac ttactcagta taatgttaac 360
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<220>
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<400> 62

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 -120 -115 -110
 Glu Leu Lys Thr Ala Phe Gly Asp Glu Glu Ile Phe Thr Asp Leu Thr
 -105 -100 -95
 Tyr His Ile His Val Asn Val Ser Gly Glu Ile Asp Ser Tyr Tyr His
 -90 -85 -80
 Asn Leu Val Asn Phe Val Asp Asn Ala Leu Ala Asn Lys Asp Ile Asn
 -75 -70 -65 -60
 Arg Tyr Ile Tyr Ala Ile Phe Thr Gln Gln Thr Asn Tyr Thr Glu Asp
 -55 -50 -45
 Gly Leu Ile Glu Tyr Leu Asn His Tyr Asp Ser Glu Thr Cys Lys Asp
 -40 -35 -30
 Ile Ile Thr Gln Tyr Asn Val Asn Val Asp Thr Ser Asn Cys Ile Ser
 -25 -20 -15
 Asn Thr Thr Asp Gln Ala Arg Leu Gln Arg Arg
 -10 -5

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 attctaaata ataaagctact cctccccccc caggagtatt tttaggggaa ggggggacct 120
 taactcaagg gggagtagtt ttgaggatca catgggaagt atttaataaa atagtagttc 180
 ttttgttta aaaaggcctc tccaaaagta atacttttag ggttaattact aagtataata 240
 tatattataa gtaatgcct ttatagctt atggtaaagc agtaaatttg agatttacct 300
 atatgttagtt cgattctcat taaggcaat ataaataagc ttttaatgg gccaatagct 360
 gaaataagta atattattgt aaatatttgag acttgaactc aaatcttatg cacctaaaaa 420
 catatatttt aaccaattaa attatattta ctttattatt tacttatata acttotacta 480
 attgtaaagt ataaccagct ttttgttta caacaaaaac cgagagggtt catgttatat 540
 ataatttata attgttctta ctttatttat aaaagaataa ccgaatg 587

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 ccccttatga gttttcatat tataaatata aaaactttt tgaggggacc tataagaaat 180
 aattgaggaa taattaataa taagttgccc tcctttttt tctttctcc ccaccctaaa 240
 aataactcctg ggggggggag ggagagaatg tatgtagtgg ggagggtgtt agttaataat 300
 agacttaaat agagttatat aaaataacat aaatatgctt aaaaataataa ataaataat 360
 taacagatag aagccaaagg gtcaggcgct ttctttggga gaaagagttt gttagttcga 420
 atctatccctt tctga 435

<210> 65
 <211> 299
 <212> DNA
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gagcttgacg gggAAAGCCG gcgaacgtgg cgagAAAGGA agggAAAGAA gcgAAAGGAG 120
cgggcgttag ggcgtggca agttagcgg tcacgtcg cgtaccacc acaccCGCCG 180
cgcttaatgc ggcgtacag ggcgtcgtacag gtggcacttt tcggggaaat gtgcgcggaa 240
ccccatatttgc ttatTTTC taaatacatt caaatatgtt tccgctcatg agacaataa 299

<210> 66
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<212> DNA
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cagaaaaaaa aatacaaATG ggataagtgc aaaacattcc atgttatctgt agcttccaat 120
gttattccctc tctccagagt caggcttctg tgt 153

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<212> DNA
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aattgatcat acataatata gatgaataag aataatgaaa ctatgtcaat aattgatcca 180
attgatgcta cataatttca accagcaaag gcatcagggt agtcaggaat t 231

<210> 68
<211> 52
<212> DNA
<213> Zygosaccharomyces bailii

<400> 68
ctcgtaaaaaa cgagcatgag ctgcgtcagg tcagccgtgg atatcgTTGC gg 52

<210> 69
<211> 116
<212> DNA
<213> Zygosaccharomyces bailii

<400> 69
ctatctgcac gtGCCACCGG aggtgctgtg ggagcgactg cggcacgatc gcatcggcc 60
gctgctgcag gtGCCGcAGC cgaggcagcg cattttcgaa ctctacgccc agcgcg 116

<210> 70
<211> 268
<212> DNA
<213> Zygosaccharomyces bailii

<400> 70
ccggcccctt gttgcgggcg gtGCCGATCA ggcgcAGCgA gttgatctcg cgcaGGCCGT 60
cctgggcata attgagcaaa tcgtactcgt gcgcggcgat ggcgtccttg ccgatcgaat 120
tgacgttaatc gatgcggcgc cggagcccga tcgcctcgac gatcggcggc gtGCCGGCCT 180
cgaacttgcg cggcgggtcg ccataggtga cccagtcctt ggcaacttca cggatcattt 240
cgccggccgc gttgaacggc cgcacatcgc 268

<210> 71
 <211> 869
 <212> DNA
 <213> Zygosaccharomyces bailii

<400> 71
 cacacagaaa cagctatgac catgatacgc caagcttaat acgactcaact atagggaaagc 60
 tcggtaccac gcatgctgca gacgcgttac gtatcggtac cagaattcgat gatattctat 120
 tgggtatgtc ccctgattcg acggcgtaaa ttgcgtgaat ctgtgttgg cgctaatgac 180
 cgcttttgg aattatgtgc tatgectctg ccattgttat caacagctga aatatttgtt 240
 gaagatcgaa tatcttctat tggttcttag ggtatccccg aagctatggc gaaagaaaagg 300
 atctcttcgtc gtacttggat cggtacgaga agcaatagac gcacaatgca ttgacgcattc 360
 ttgttgcata cgggtaatgt gagttctctg gggtctgtta ttgagttaa tatgtcgtcc 420
 acctctgttc tctgtatccat tttgcgagta gcccgcata cagcacgtcc aatacaggag 480
 agggcattta gcttcaggtg cagagaagac acagcatggt gtcacccctc gagtgctca 540
 atagatgatt gagttgactg ggcttcgtg aaagggcctt tccagagatc ttcaaaaaata 600
 aaccagggtt gcgcttcatt agtaggtgtt cctggaggac tattgtcgct atctgctgga 660
 ctactgtcac caagtagtga agggggattt ctaaggcttt cactctgttc tgacactatt 720
 ataacattgc caaggccaat ttgaaagggtt tcgcgtatat gagtaaagag ctcggtgccc 780
 ttccagttgg aatcaagccg ttcaagcaga tcgagagcat aatcagagtc cacattccg 840
 cacgcaagag agaactctga gttcattct 869

<210> 72
 <211> 1425
 <212> DNA
 <213> Zygosaccharomyces bailii

<220>
 <221> CDS
 <222> (1)...(1425)

<400> 72
 atg tcc gag ttt agc gag ctt gtc aga att ctc cca tta gac cag gtt 48
 Met Ser Glu Phe Ser Glu Leu Val Arg Ile Leu Pro Leu Asp Gln Val
 1 5 10 15

gca gaa ata aag cgt att ttg agt cgc ggc gac cct ata cct tta caa 96
 Ala Glu Ile Lys Arg Ile Leu Ser Arg Gly Asp Pro Ile Pro Leu Gln
 20 25 30

agg tta gct tct cta cta act atg gtg atc cta acg gtc aac atg tca 144
 Arg Leu Ala Ser Leu Leu Thr Met Val Ile Leu Thr Val Asn Met Ser
 35 40 45

aaa aag agg aag agc tct cca atc aag ctt agc acc ttt act aaa tat 192
 Lys Lys Arg Lys Ser Ser Pro Ile Lys Leu Ser Thr Phe Thr Lys Tyr
 50 55 60

cgt aga aat gtt gcg aag tca ttg tat tat gat atg tca agc aag aca 240
 Arg Arg Asn Val Ala Lys Ser Leu Tyr Tyr Asp Met Ser Ser Lys Thr
 65 70 75 80

gta ttc ttc gaa tac cat ctc aaa aat aca caa gat cta cag gag ggc 288
 Val Phe Phe Glu Tyr His Leu Lys Asn Thr Gln Asp Leu Gln Glu Gly
 85 90 95

ctc gag caa gcc att gcg ccc tac aat ttc gtg gta aag gtg cac aag 336

Leu Glu Gln Ala Ile Ala Pro Tyr Asn Phe Val Val Lys Val His Lys			
100	105	110	
aag cca att gat tgg cag aaa cag ctc tca agc gtg cat gag agg aaa			384
Lys Pro Ile Asp Trp Gln Lys Gln Leu Ser Ser Val His Glu Arg Lys			
115	120	125	
gcg ggc cac aga agc att ctc agc aac aat gtt ggc gcc gag atc tct			432
Ala Gly His Arg Ser Ile Leu Ser Asn Asn Val Gly Ala Glu Ile Ser			
130	135	140	
aaa ctg gct gag acg aaa gat tct act tgg agt ttt atc gag aga aca			480
Lys Leu Ala Glu Thr Lys Asp Ser Thr Trp Ser Phe Ile Glu Arg Thr			
145	150	155	160
atg gat ctg ata gaa gcc cgc acc cgc cag ccc acg aca aga gtt gcg			528
Met Asp Leu Ile Glu Ala Arg Thr Arg Gln Pro Thr Thr Arg Val Ala			
165	170	175	
tat agg ttt ctg ctt caa ctc aca ttc atg aac tgc tgt agg gct aat			576
Tyr Arg Phe Leu Leu Gln Leu Thr Phe Met Asn Cys Cys Arg Ala Asn			
180	185	190	
gat ttg aaa aac gcc gac ccc agc act ttt caa atc atc gca gat cct			624
Asp Leu Lys Asn Ala Asp Pro Ser Thr Phe Gln Ile Ile Ala Asp Pro			
195	200	205	
cac ctt ggt cgt ata ttg cg ^g gcc ttt gtt cca gag aca aag act agc			672
His Leu Gly Arg Ile Leu Arg Ala Phe Val Pro Glu Thr Lys Thr Ser			
210	215	220	
att gaa agg ttt atc tat ttt ttc cca tgt aag gga cga tgc gat ccg			720
Ile Glu Arg Phe Ile Tyr Phe Pro Cys Lys Gly Arg Cys Asp Pro			
225	230	235	240
ctt ttg gct cta gat tcc tat ctc ctg tgg gtt ggc cca gtg ccc aaa			768
Leu Leu Ala Leu Asp Ser Tyr Leu Leu Trp Val Gly Pro Val Pro Lys			
245	250	255	
act cag act acc gat gaa gag act caa tat gat tac cag ctt ctt caa			816
Thr Gln Thr Asp Glu Glu Thr Gln Tyr Asp Tyr Gln Leu Leu Gln			
260	265	270	
gat act ctc ttg att tcg tac gac agg ttt atc gcc aaa gaa tca aag			864
Asp Thr Leu Leu Ile Ser Tyr Asp Arg Phe Ile Ala Lys Glu Ser Lys			
275	280	285	
gaa aat att ttc aaa ata cct aat ggg ccc aaa gct cat ttg ggg cg ^g			912
Glu Asn Ile Phe Lys Ile Pro Asn Gly Pro Lys Ala His Leu Gly Arg			
290	295	300	
cat cta atg gca tca tac ctt gga aac aac agt ctc aag agc gag gcc			960
His Leu Met Ala Ser Tyr Leu Gly Asn Asn Ser Leu Lys Ser Glu Ala			
305	310	315	320
aca ctc tac ggc aac tgg tct gtg gaa agg caa gag ggc gtc agc aaa			1008
Thr Leu Tyr Gly Asn Trp Ser Val Glu Arg Gln Glu Gly Val Ser Lys			

21/31

325

330

335

atg gct gac agc cga tac atg cac acg gtt aaa aaa agt cca cct tca Met Ala Asp Ser Arg Tyr Met His Thr Val Lys Lys Ser Pro Pro Ser 340 345 350	1056
tat cta ttt gca ttt tta tcc ggc tac tac aaa aag tcc aac caa ggc Tyr Leu Phe Ala Phe Leu Ser Gly Tyr Tyr Lys Lys Ser Asn Gln Gly 355 360 365	1104
gag tac gtg ctg gct gaa aca ctg tat aat ccc ctg gat tac gac aaa Glu Tyr Val Leu Ala Glu Thr Leu Tyr Asn Pro Leu Asp Tyr Asp Lys 370 375 380	1152
aca ctt cca ata aca acg aac gag aaa ttg atc tgt cgg cg ^g tac ggg Thr Leu Pro Ile Thr Asn Glu Lys Leu Ile Cys Arg Arg Tyr Gly 385 390 395 400	1200
aaa aat gcg aaa gtg ata cca aaa gac gca ctg ctg tat ctc tac acg Lys Asn Ala Lys Val Ile Pro Lys Asp Ala Leu Leu Tyr Leu Tyr Thr 405 410 415	1248
tat gcg cag cag aag cga aaa caa ttg gcc gat ccc aat gag caa aat Tyr Ala Gln Gln Lys Arg Lys Gln Leu Ala Asp Pro Asn Glu Gln Asn 420 425 430	1296
agg cta ttc agt agt gaa tca cca gcg cat ccc ttc tta act cct caa Arg Leu Phe Ser Ser Glu Ser Pro Ala His Pro Phe Leu Thr Pro Gln 435 440 445	1344
tcg aca ggc tca tcg aca ccc ttg acc tgg act gct cca aag aca ctc Ser Thr Gly Ser Ser Thr Pro Leu Thr Trp Thr Ala Pro Lys Thr Leu 450 455 460	1392
tcc act ggt cta atg aca cct gga gaa gag tag Ser Thr Gly Leu Met Thr Pro Gly Glu Glu * 465 470	1425

<210> 73
<211> 474
<212> PRT
<213> Zygosaccharomyces bailii

<400> 73	
Met Ser Glu Phe Ser Glu Leu Val Arg Ile Leu Pro Leu Asp Gln Val	
1 5 10 15	
Ala Glu Ile Lys Arg Ile Leu Ser Arg Gly Asp Pro Ile Pro Leu Gln	
20 25 30	
Arg Leu Ala Ser Leu Leu Thr Met Val Ile Leu Thr Val Asn Met Ser	
35 40 45	
Lys Lys Arg Lys Ser Ser Pro Ile Lys Leu Ser Thr Phe Thr Lys Tyr	
50 55 60	
Arg Arg Asn Val Ala Lys Ser Leu Tyr Tyr Asp Met Ser Ser Lys Thr	
65 70 75 80	
Val Phe Phe Glu Tyr His Leu Lys Asn Thr Gln Asp Leu Gln Glu Gly	
85 90 95	

Leu Glu Gln Ala Ile Ala Pro Tyr Asn Phe Val Val Lys Val His Lys
 100 105 110
 Lys Pro Ile Asp Trp Gln Lys Gln Leu Ser Ser Val His Glu Arg Lys
 115 120 125
 Ala Gly His Arg Ser Ile Leu Ser Asn Asn Val Gly Ala Glu Ile Ser
 130 135 140
 Lys Leu Ala Glu Thr Lys Asp Ser Thr Trp Ser Phe Ile Glu Arg Thr
 145 150 155 160
 Met Asp Leu Ile Glu Ala Arg Thr Arg Gln Pro Thr Thr Arg Val Ala
 165 170 175
 Tyr Arg Phe Leu Leu Gln Leu Thr Phe Met Asn Cys Cys Arg Ala Asn
 180 185 190
 Asp Leu Lys Asn Ala Asp Pro Ser Thr Phe Gln Ile Ile Ala Asp Pro
 195 200 205
 His Leu Gly Arg Ile Leu Arg Ala Phe Val Pro Glu Thr Lys Thr Ser
 210 215 220
 Ile Glu Arg Phe Ile Tyr Phe Phe Pro Cys Lys Gly Arg Cys Asp Pro
 225 230 235 240
 Leu Leu Ala Leu Asp Ser Tyr Leu Leu Trp Val Gly Pro Val Pro Lys
 245 250 255
 Thr Gln Thr Thr Asp Glu Glu Thr Gln Tyr Asp Tyr Gln Leu Leu Gln
 260 265 270
 Asp Thr Leu Ile Ser Tyr Asp Arg Phe Ile Ala Lys Glu Ser Lys
 275 280 285
 Glu Asn Ile Phe Lys Ile Pro Asn Gly Pro Lys Ala His Leu Gly Arg
 290 295 300
 His Leu Met Ala Ser Tyr Leu Gly Asn Asn Ser Leu Lys Ser Glu Ala
 305 310 315 320
 Thr Leu Tyr Gly Asn Trp Ser Val Glu Arg Gln Glu Gly Val Ser Lys
 325 330 335
 Met Ala Asp Ser Arg Tyr Met His Thr Val Lys Lys Ser Pro Pro Ser
 340 345 350
 Tyr Leu Phe Ala Phe Leu Ser Gly Tyr Tyr Lys Lys Ser Asn Gln Gly
 355 360 365
 Glu Tyr Val Leu Ala Glu Thr Leu Tyr Asn Pro Leu Asp Tyr Asp Lys
 370 375 380
 Thr Leu Pro Ile Thr Thr Asn Glu Lys Leu Ile Cys Arg Arg Tyr Gly
 385 390 395 400
 Lys Asn Ala Lys Val Ile Pro Lys Asp Ala Leu Leu Tyr Leu Tyr Thr
 405 410 415
 Tyr Ala Gln Gln Lys Arg Lys Gln Leu Ala Asp Pro Asn Glu Gln Asn
 420 425 430
 Arg Leu Phe Ser Ser Glu Ser Pro Ala His Pro Phe Leu Thr Pro Gln
 435 440 445
 Ser Thr Gly Ser Ser Thr Pro Leu Thr Trp Thr Ala Pro Lys Thr Leu
 450 455 460
 Ser Thr Gly Leu Met Thr Pro Gly Glu Glu
 465 470

<210> 74
 <211> 1075
 <212> DNA
 <213> Zygosaccharomyces bailii

<220>
 <221> CDS

<222> (1)...(1074)

<400> 74

atg ttc tcc agg gaa gag gtt agg gcc tcc agg ccc act aaa gag atg	48
Met Phe Ser Arg Glu Glu Val Arg Ala Ser Arg Pro Thr Lys Glu Met	
1 5 10 15	
aag atg atc ttt gat gtg ctt atg aca ttt cct tac ttc gcg gta cat	96
Lys Met Ile Phe Asp Val Leu Met Thr Phe Pro Tyr Phe Ala Val His	
20 25 30	
gtt cct tcc aag aat ata ctt atc aca cca aaa ggc aca gtt gag ata	144
Val Pro Ser Lys Asn Ile Leu Ile Thr Pro Lys Gly Thr Val Glu Ile	
35 40 45	
cct gaa aac tat caa aat tat ccc ata ttg gcc atc ttc tac gtc aaa	192
Pro Glu Asn Tyr Gln Asn Tyr Pro Ile Leu Ala Ile Phe Tyr Val Lys	
50 55 60	
tat tta atg aag aaa aat ccg tac gat ctt ctt cca agc acc gtg aac	240
Tyr Leu Met Lys Lys Asn Pro Tyr Asp Leu Leu Pro Ser Thr Val Asn	
65 70 75 80	
tgg ccg gaa ccc tat gta gtg gtg aat acc atc act aag cgt ttc cag	288
Trp Pro Glu Pro Tyr Val Val Val Asn Thr Ile Thr Lys Arg Phe Gln	
85 90 95	
gac cat aaa cta ttt gca aac aaa aat gct gat gtc tac gtt gaa aga	336
Asp His Lys Leu Phe Ala Asn Lys Asn Ala Asp Val Tyr Val Glu Arg	
100 105 110	
ctt caa aat gca att gcc tcg ggt att aag att cct gag tct aag aag	384
Leu Gln Asn Ala Ile Ala Ser Gly Ile Lys Ile Pro Glu Ser Lys Lys	
115 120 125	
aat gaa cga tta ggg cag cca aaa aag acg aaa aat gtt aca aaa gag	432
Asn Glu Arg Leu Gly Gln Pro Lys Lys Thr Lys Asn Val Thr Lys Glu	
130 135 140	
aat tga gga gac ctt tat tga tgc cac taa tgc gag aaa aga att gga	480
Asn * Gly Asp Leu Tyr * Cys His * Cys Glu Lys Arg Ile Gly	
145 150 155	
tga gta ctt cag aaa act tca gga tgg tac att aac cgg aga ttt gga	528
* Val Leu Gln Lys Thr Ser Gly Trp Tyr Ile Asn Arg Arg Phe Gly	
160 165 170	
ggg tgg ctt gtg caa ggt caa aac gct cat atc gtg taa agc ttt gtt	576
Gly Trp Leu Val Gln Gly Gln Asn Ala His Ile Val * Ser Phe Val	
175 180 185	
cgg agg aca cac cca aga act cca gtt tat ggc cac caa tgt tcg taa	624
Arg Arg Thr His Pro Arg Thr Pro Val Tyr Gly His Gln Cys Ser *	
190 195 200	
agt ctg gat agg gga gat agt gtg cgg cat ggt ttc caa taa aaa tgc	672
Ser Leu Asp Arg Gly Asp Ser Val Arg His Gly Phe Gln * Lys Cys	

205	210	215	
aat tga cga taa tga tct cga gga aga aga gcg taa tgc atc ggg cga Asn * Arg * * Ser Arg Gly Arg Arg Ala * Cys Ile Gly Arg 220 225			720
aca aac tac gac agc ccg aga gga atc aga ggc tct gga tac cac atc Thr Asn Tyr Asp Ser Pro Arg Gly Ile Arg Gly Ser Gly Tyr His Ile 230 235 240 245			768
caa tgg ttt gga cgc tct gaa tac tca aat taa tgc cat aga aac gga Gln Trp Phe Gly Arg Ser Glu Tyr Ser Asn * Cys His Arg Asn Gly 250 255 260			816
gga atc att ttg gga agc tat cag ggc gct cca taa tga gct acg cac Gly Ile Ile Leu Gly Ser Tyr Gln Gly Ala Pro * * Ala Thr His 265 270			864
ctc tcc aac aca gtt aga aga gtg cag gaa agc ggc agt ttt ttt act Leu Ser Asn Thr Val Arg Arg Val Gln Glu Ser Gly Ser Phe Phe Thr 275 280 285 290			912
ggg cca taa aaa aat act cca aac att tac aaa gca aaa gga tac tgc Gly Pro * Lys Asn Thr Pro Asn Ile Tyr Lys Ala Lys Gly Tyr Cys 295 300 305			960
ccg cgc tct ttt tta tat aaa tct caa aga gtg tct ggg aac cag ctg Pro Arg Ser Phe Leu Tyr Lys Ser Gln Arg Val Ser Gly Asn Gln Leu 310 315 320			1008
gaa ttt aga ata tac aga ggc atc aga tgc aag aaa aat ggc aat taa Glu Phe Arg Ile Tyr Arg Gly Ile Arg Cys Lys Lys Asn Gly Asn * 325 330 335			1056
agg tga gct tca aaa tta a Arg * Ala Ser Lys Leu 340			1075

<210> 75
<211> 341
<212> PRT
<213> Zygosaccharomyces bailii

<400> 75
Met Phe Ser Arg Glu Glu Val Arg Ala Ser Arg Pro Thr Lys Glu Met
1 5 10 15
Lys Met Ile Phe Asp Val Leu Met Thr Phe Pro Tyr Phe Ala Val His
20 25 30
Val Pro Ser Lys Asn Ile Leu Ile Thr Pro Lys Gly Thr Val Glu Ile
35 40 45
Pro Glu Asn Tyr Gln Asn Tyr Pro Ile Leu Ala Ile Phe Tyr Val Lys
50 55 60
Tyr Leu Met Lys Lys Asn Pro Tyr Asp Leu Leu Pro Ser Thr Val Asn
65 70 75 80
Trp Pro Glu Pro Tyr Val Val Val Asn Thr Ile Thr Lys Arg Phe Gln
85 90 95

Asp His Lys Leu Phe Ala Asn Lys Asn Ala Asp Val Tyr Val Glu Arg
 100 105 110
 Leu Gln Asn Ala Ile Ala Ser Gly Ile Lys Ile Pro Glu Ser Lys Lys
 115 120 125
 Asn Glu Arg Leu Gly Gln Pro Lys Lys Thr Lys Asn Val Thr Lys Glu
 130 135 140
 Asn Gly Asp Leu Tyr Cys His Cys Glu Lys Arg Ile Gly Val Leu Gln
 145 150 155 160
 Lys Thr Ser Gly Trp Tyr Ile Asn Arg Arg Phe Gly Gly Trp Leu Val
 165 170 175
 Gln Gly Gln Asn Ala His Ile Val Ser Phe Val Arg Arg Thr His Pro
 180 185 190
 Arg Thr Pro Val Tyr Gly His Gln Cys Ser Ser Leu Asp Arg Gly Asp
 195 200 205
 Ser Val Arg His Gly Phe Gln Lys Cys Asn Arg Ser Arg Gly Arg Arg
 210 215 220
 Ala Cys Ile Gly Arg Thr Asn Tyr Asp Ser Pro Arg Gly Ile Arg Gly
 225 230 235 240
 Ser Gly Tyr His Ile Gln Trp Phe Gly Arg Ser Glu Tyr Ser Asn Cys
 245 250 255
 His Arg Asn Gly Gly Ile Ile Leu Gly Ser Tyr Gln Gly Ala Pro Ala
 260 265 270
 Thr His Leu Ser Asn Thr Val Arg Arg Val Gln Glu Ser Gly Ser Phe
 275 280 285
 Phe Thr Gly Pro Lys Asn Thr Pro Asn Ile Tyr Lys Ala Lys Gly Tyr
 290 295 300
 Cys Pro Arg Ser Phe Leu Tyr Lys Ser Gln Arg Val Ser Gly Asn Gln
 305 310 315 320
 Leu Glu Phe Arg Ile Tyr Arg Gly Ile Arg Cys Lys Lys Asn Gly Asn
 325 330 335
 Arg Ala Ser Lys Leu
 340

<210> 76
 <211> 750
 <212> DNA
 <213> Zygosaccharomyces bailii

<220>
 <221> CDS
 <222> (1)...(750)

<400> 76
 atg aac tca gag ttc tct ctt gcg tac gga aat gtg gac tct gat tat 48
 Met Asn Ser Glu Phe Ser Leu Ala Tyr Gly Asn Val Asp Ser Asp Tyr
 1 5 10 15
 gct ctc gat ctg ctt gaa cgg ctt gat tcc aac tgg aag ggc acc gag 96
 Ala Leu Asp Leu Leu Glu Arg Leu Asp Ser Asn Trp Lys Gly Thr Glu
 20 25 30
 ctc ttt act cat ata cgc gaa acc ttt caa att ggc ctt ggc aat gtt 144
 Leu Phe Thr His Ile Arg Glu Thr Phe Gln Ile Gly Leu Gly Asn Val
 35 40 45
 atc ata gtg tca gaa cag agt gaa agc ctt aga ata ccc cct tca cta 192

Ile Ile Val Ser Glu Gln Ser Glu Ser Leu Arg Ile Pro Pro Ser Leu			
50	55	60	
ctt ggt agc agt agt cca gca gat agc gac aat agt cct cca gga aca	240		
Leu Gly Ser Ser Ser Pro Ala Asp Ser Asp Asn Ser Pro Pro Gly Thr			
65	70	75	80
cct act aat gaa gcg caa ccc tgg ttt att tct gaa gat ctc tcg aaa	288		
Pro Thr Asn Glu Ala Gln Pro Trp Phe Ile Ser Glu Asp Leu Ser Lys			
85	90	95	
ggc cct ttc acg gaa gcc cag tca act caa tca tct att gag aca ctc	336		
Gly Pro Phe Thr Glu Ala Gln Ser Thr Gln Ser Ser Ile Glu Thr Leu			
100	105	110	
gaa ggt gag cac cat gct gtg tct tct ctg cac ctg aag cta aat ggc	384		
Glu Gly Glu His His Ala Val Ser Ser Leu His Leu Lys Leu Asn Gly			
115	120	125	
ctc tcc tgt att gga cgt gct gta tgg cggt gct act cgc aaa atg gat	432		
Leu Ser Cys Ile Gly Arg Ala Val Trp Arg Ala Thr Arg Lys Met Asp			
130	135	140	
acg aga aca gag gtg gac gac ata tta aac tca ata aca gaa ccc aga	480		
Thr Arg Thr Glu Val Asp Asp Ile Leu Asn Ser Ile Thr Glu Pro Arg			
145	150	155	160
aga ctc aca tta ccc ggt atc aac aag atg cgt caa tgc att gtg cgt	528		
Arg Leu Thr Leu Pro Gly Ile Asn Lys Met Arg Gln Cys Ile Val Arg			
165	170	175	
cta ttg ctt ctc gta ccg atc caa gta cga gaa gag atc ctt tct ttc	576		
Leu Leu Leu Val Pro Ile Gln Val Arg Glu Glu Ile Leu Ser Phe			
180	185	190	
gcc ata gct tcg ggg ata ccc tca gaa aca ata gaa gat att cga tct	624		
Ala Ile Ala Ser Gly Ile Pro Ser Glu Thr Ile Glu Asp Ile Arg Ser			
195	200	205	
tca aca aat att tca gct gtt gat acc aat ggc aga ggc ata gca cat	672		
Ser Thr Asn Ile Ser Ala Val Asp Thr Asn Gly Arg Gly Ile Ala His			
210	215	220	
aat tcc aaa aag cgg tca tta gcg cca aca caa gat tca cgc aat tta	720		
Asn Ser Lys Lys Arg Ser Leu Ala Pro Thr Gln Asp Ser Arg Asn Leu			
225	230	235	240
cgc cgt cga atc agg gga cat acc caa tag	750		
Arg Arg Arg Ile Arg Gly His Thr Gln *			
245			

<210> 77
<211> 249
<212> PRT
<213> Zygosaccharomyces bailii

<400> 77

Met	Asn	Ser	Glu	Phe	Ser	Leu	Ala	Tyr	Gly	Asn	Val	Asp	Ser	Asp	Tyr
1			5					10				15			
Ala	Leu	Asp	Leu	Leu	Glu	Arg	Leu	Asp	Ser	Asn	Trp	Lys	Gly	Thr	Glu
	20							25				30			
Leu	Phe	Thr	His	Ile	Arg	Glu	Thr	Phe	Gln	Ile	Gly	Leu	Gly	Asn	Val
	35					40				45					
Ile	Ile	Val	Ser	Glu	Gln	Ser	Glu	Ser	Leu	Arg	Ile	Pro	Pro	Ser	Leu
	50					55				60					
Leu	Gly	Ser	Ser	Pro	Ala	Asp	Ser	Asp	Asn	Ser	Pro	Pro	Gly	Thr	
	65				70			75			80				
Pro	Thr	Asn	Glu	Ala	Gln	Pro	Trp	Phe	Ile	Ser	Glu	Asp	Leu	Ser	Lys
						85		90			95				
Gly	Pro	Phe	Thr	Glu	Ala	Gln	Ser	Thr	Gln	Ser	Ser	Ile	Glu	Thr	Leu
						100		105			110				
Glu	Gly	Glu	His	His	Ala	Val	Ser	Ser	Leu	His	Leu	Lys	Leu	Asn	Gly
						115		120			125				
Leu	Ser	Cys	Ile	Gly	Arg	Ala	Val	Trp	Arg	Ala	Thr	Arg	Lys	Met	Asp
						130		135			140				
Thr	Arg	Thr	Glu	Val	Asp	Asp	Ile	Leu	Asn	Ser	Ile	Thr	Glu	Pro	Arg
	145					150			155			160			
Arg	Leu	Thr	Leu	Pro	Gly	Ile	Asn	Lys	Met	Arg	Gln	Cys	Ile	Val	Arg
						165		170			175				
Leu	Leu	Leu	Val	Pro	Ile	Gln	Val	Arg	Glu	Glu	Ile	Leu	Ser	Phe	
						180		185			190				
Ala	Ile	Ala	Ser	Gly	Ile	Pro	Ser	Glu	Thr	Ile	Glu	Asp	Ile	Arg	Ser
						195		200			205				
Ser	Thr	Asn	Ile	Ser	Ala	Val	Asp	Thr	Asn	Gly	Arg	Gly	Ile	Ala	His
						210		215			220				
Asn	Ser	Lys	Lys	Arg	Ser	Leu	Ala	Pro	Thr	Gln	Asp	Ser	Arg	Asn	Leu
						225		230			235			240	
Arg	Arg	Arg	Ile	Arg	Gly	His	Thr	Gln							
					245										

<210> 78
<211> 453
<212> DNA
<213> *Saccharomyces cerevisiae*

<220>
<221> promoter
<222> (1)...(450)

<221> misc_feature
<222> (451)...(453)
<223> start codon

<400> 78

ctacttattc	ccttcgagat	tatacttagg	aacccatcg	gttggtgaa	gattaccgt	60
tctaagactt	ttcagcttcc	tctattgtat	ttacacctgg	acaccccttt	tctggcatcc	120
agtttttaat	cttcagtgcc	atgtgagatt	ctccgaaatt	aattaaagca	atcacacaat	180
tctctcgat	accacctcg	ttgaaactga	caggtggttt	gttacgcatg	ctaatgc当地	240
ggagcctata	tacctttggc	tcggctgtcg	taacaggaa	tataaagggc	agcataattt	300
aggagtttag	tgaacttgca	acatttacta	ttttcccttc	ttacgtaaat	atttttcttt	360
ttaattctaa	atcaatctt	ttcaattttt	tggttgtatt	ctttcttgc	ttaaatctat	420
aactacaaaa	aacacataca	taaactaaaa	atg			453

<210> 79
 <211> 499
 <212> DNA
 <213> Zygosaccharomyces bailii

<220>
 <221> promoter
 <222> (1)...(496)

<221> misc_feature
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 cgtgtatcca tttgatactg tgctggttac aagacacatg ctttacaagg acacttctat 180
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 cattatttt ccctttact tccgtcacgc cggggctcca ctttttggg ttccactttt 300
 cttacgaccc tcgacatcca ctaaacgaac aggaagtcaa agaacccttc gagtcacacg 360
 gtgcgttatgc gctgttaaca tatataaagg tcaccttcc ctgctaaaaa gagtcttagc 420
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